

1	TTACCAGAACAGCATAACAAGGGCAGGTCTGACTGCAAGCTGGGACTGGGAGGCAGAGCC	60
61	GCCGCCAAGGGGGCCTCGGTAAACACTGGTCGTTCAATCACCTGCAAGACGAAGAGGCA	120
121	AGGATGCTGTTGGCCTGGGTACAAGCATTCTCGTCAGCAACATGCTCCTAGCAGAAGCC	180
1	<u>M L L A W V Q A F L V S N M L L A E A</u>	19
181	TATGGATCTGGAGGCTGTTTCTGGGACAACGGCCACCTGTACCGGGAGGACCAGACCTCC	240
20	<u>Y G</u> S G G C F W D N G H L Y R E D Q T S	39
241	CCCGCGCCGGGCCTCCGCTGCCTCAACTGGCTGGACGCGCAGAGCGGGCTGGCCTCGGCC	300
40	P A P G L R C L N W L D A Q S G L A S A	59
301	CCCGTGTGCGGGGCGGCAATCACAGTTACTGCCGAAACCCGGACGAGGACCCGCGCGGG	360
60	P V S G A G N H S Y C R N P D E D P R G	79
361	CCCTGGTGCTACGTCACTGGCGAGGCCGGCGTCCCTGAGAAACGGCCTTGCGAGGACCTG	420
80	P W C Y V S G E A G V P E K R P C E D L	99
421	CGCTGTCCAGAGACCACCTCCCAGGCCCTGCCAGCCTTCACGACAGAAATCCAGGAAGCG	480
100	R C P E T T S Q A L P A F T T E I Q E A	119
481	TCTGAAGGGCCAGGTGCAGATGAGGTGCAGGTGTTGCTCCTGCCAACGCCCTGCCCCTG	540
120	S E G P G A D E V Q V F A P A N A L P A	139
541	CGGAGTGAGGCGGCAGCTGTGCAGCCAGTGATTGGGATCAGCCAGCGGGTGCGGATGAAC	600
140	R S E A A A V Q P V I G I S Q R V R M N	159
601	TCCAAGGAGAAAAAGGACCTGGGAACCTCTGGGCTACGTGCTGGGCATTACCATGATGGTG	660
160	S K E K K D L G T L G Y V L G I T M M V	179
661	ATCATCATTGCCATCGGAGCTGGCATCATCTTGGGCTACTCCTACAAGAGGGGGAAGGAT	720
180	I I I A I G A G I I L G Y S Y K R G K D	199

FIG.1A

721	TTGAAAGAACAGCATGATCAGAAAGTATGTGAGAGGGAGATGCAGCGAATCACTCTGCCC	780
200	L K E Q H D Q K V C E R E M Q R I T L P	219
781	TTGTCTGCCTTCACCAACCCACCTGTGAGATTGTGGATGAGAAGACTGTCGTGGTCCAC	840
220	L S A F T N P T C E I V D E K T V V V H	239
841	ACCAGCCAGACTCCAGTTGACCCTCAGGAGGGCAGCACCCCTTATGGGCCAGGCCGGG	900
240	T S Q T P V D P Q E G S T P L M G Q A G	259
901	ACTCCTGGGGCCTGAGCCCCCAGTGGGCAGGAGCCCATGCAGACACTGGTGCAGGACA	960
260	T P G A *	263
961	GCCCACCCTCCTACAGCTAGGAGGAACTACCACTTTGTGTTCTGGTTAAAACCCTACCAC	1020
1021	TCCCCGCTTTTTTGGCGAATCCTAGTAAGAGTGACAGAAGCAGGTGGCCCTGTGGGCTG	1080
1081	AGGGTAAGGCTGGGTAGGGTCCTAACAGTGCTCCTTGTCATCCCTTGGAGCAGATTTTG	1140
1141	TCTGTGGATGGAGACAGTGGCAGCTCCACAGTGATGCTGCTGCTAAGGGCTTCCAAACA	1200
1201	TTGCCTGCACCCCTGGAACCTGAACCAGGGATAGACGGGGAGCTCCCCCAGGCTCCTCTGT	1260
1261	GCTTTACTAAGATGGCTCAGTCTCCACTGTGGGCTTGAGTGGCATACACTGTTATTCATG	1320
1321	GTTAAGGTAAAGCAGGTCAAGGGATGGCATTGAAAAAATATATTTAGTTTTTAAATATT	1380
1381	TGGGATGGAACCTCCCTACTGACCTCTGACAACTGGAAACGAGTTTGTACTGAAGTCAGAA	1440
1441	CTTTGGGTTGGGAATGAGATCTAGGTTGTGGCTGCTGGTATGCTTCAGCTTGCTGGCAAT	1500
1501	GATGTGCCTTGACAACCGTGGGCCAGGCCTGGGCCCAGGGACTCTCCTGTTTCATAAGG	1560

FIG.1B

1561	AAAGGAAGAATTGCACTGAGCATTCCACTTAGGAAGAGGATAGAGAAGGATCTGCTCCGC	1620
1621	CTTTGGCCACAGGAGCAGAGGCAGACCTGGGATGCCCCAGTTTCTCTTCAGGGATGGATA	1680
1681	GTGACCTGTCTTCATTTTGACAGGTAAGAGAGTAGTTAGCTAACCTATGGGAATTATAC	1740
1741	TGTGGGGCCTTGTGAGCTGCTTCTAAGAGGCTAACCTGGAACTAAGCTCAGAGGCAAGG	1800
1801	TAATAAAGCACTTCAGGGCTTGCTCCCCAAGTGGGCTGATTTAGCAGGTGGTCTGCGGG	1860
1861	CGTCCAGGTCAGCACCTTCCTGTAGGGCACTGGGGCTAGGGTCACAGCCCCTAACTCATAC	1920
1921	AAGCAATCAAAGAACCATTAGAAAGGGCTCATTAAAGCCTTTTGGACACAGGACCCAGAG	1980
1981	AGGAAAAAGTGACTTGCCCAAGGTCGTAAGCAAGCTACTGGCATGGCAAGAGCCCAGCTT	2040
2041	CCTGACGGAGCGCAACATTTCTCCACTGCACTGTGCTAGCAGCTCAGCAGGGCCTCTAAC	2100
2101	CTGTGATGTCACACTCAAGAGGCCTTGGCAGCTCCTAGCCATAGAGCTTCCTTTCCAGAA	2160
2161	CCCTTCCACTGCCCAATGTGGAGACAGGGGTTAGTGGGGCTTTCTATGGAGCCATCTGCT	2220
2221	TTGGGGACCTAGACCTCAGGTGGTCTCTTGGTGTAGTGATGCTGGAGAAGAGAATATTA	2280
2281	CTGGTTTCTACTTTTCTATAAAGGCATTTCTCTATAAAAAAAAAAAAAA	2329

FIG.1C

3 LAWVQAFLVSNMLLAEAY..GSGGCFWDNGHLYREDQTSPAPGLRCLNW. 49  
 ... : : | : : ..| : | : :| : :| | : : : ..| .| | |  
 191 YVFKAGKYSSEFCSTPACSEGNSDCYFGNGSAYRGTHSLTESGASCLPWN 240  
 50 .....LDAQSGLASAPVSGAGNHSYCRNPDEDPRGPWCYV..... 84  
 ..| | . :| | . | | .| | | | | :| : : | | | .|  
 241 SMILIGKVYTAQN..PSAQUALGLGKHNYCRNPDGDAK.PWCHVLKNRRLT 287  
 85 SGEAGVPEKRPCEDLRCPETTSQALPAFTTEIQE.....ASEGPGAD 126  
 . : : :| | . ..| : : : : . : : : :| .. : : : :| .. : : : :  
 288 WEYCDVPSCSTCGLRQYSQPQFRIKGGLFADIASHPWQAAIFAKHRRSPG 337  
 127 E.....VQVFAPANALPARSEAAAVQPVIGISQRVRMNSKEK.. 163  
 | : : :| : : :| : : : :| . | | ...| .  
 338 ERFLCGGILISSCWILSAAHCFQERFPPHLLTVILGRTYRVVPGEEEQKF 387  
 164 .....KDLGTLGYVLGITMMVIIAIG....AGIILGYSYKRGKDL. 200  
 | : : : . | : | : : : : : : : : : : : : : : | |  
 388 EVEKYIVHKEFDODTYDNDIALQLKSDSSRCAQESSVVRTVCLPPADLQ 437  
 201 .....KEQHDQKVCEREMQRITLPLSAFTNPTCEIVDEKTV. 236  
 | : : : : : : : : : :| : : :| : : : :| : : : :| : : : :|  
 438 LPDWTECELSGYGKHEALSPFYSERLKEAHVRLYPSSRCTSQHLLNRTVT 487  
 237 ..VVHTSQTPVDPQEGSTPLMGQAGTPGA 263  
 : : : :| . : : : : . | : : :| :  
 488 DNMLCAGDTRSGGPQANLHDACQGDSGGP 516

FIG.2

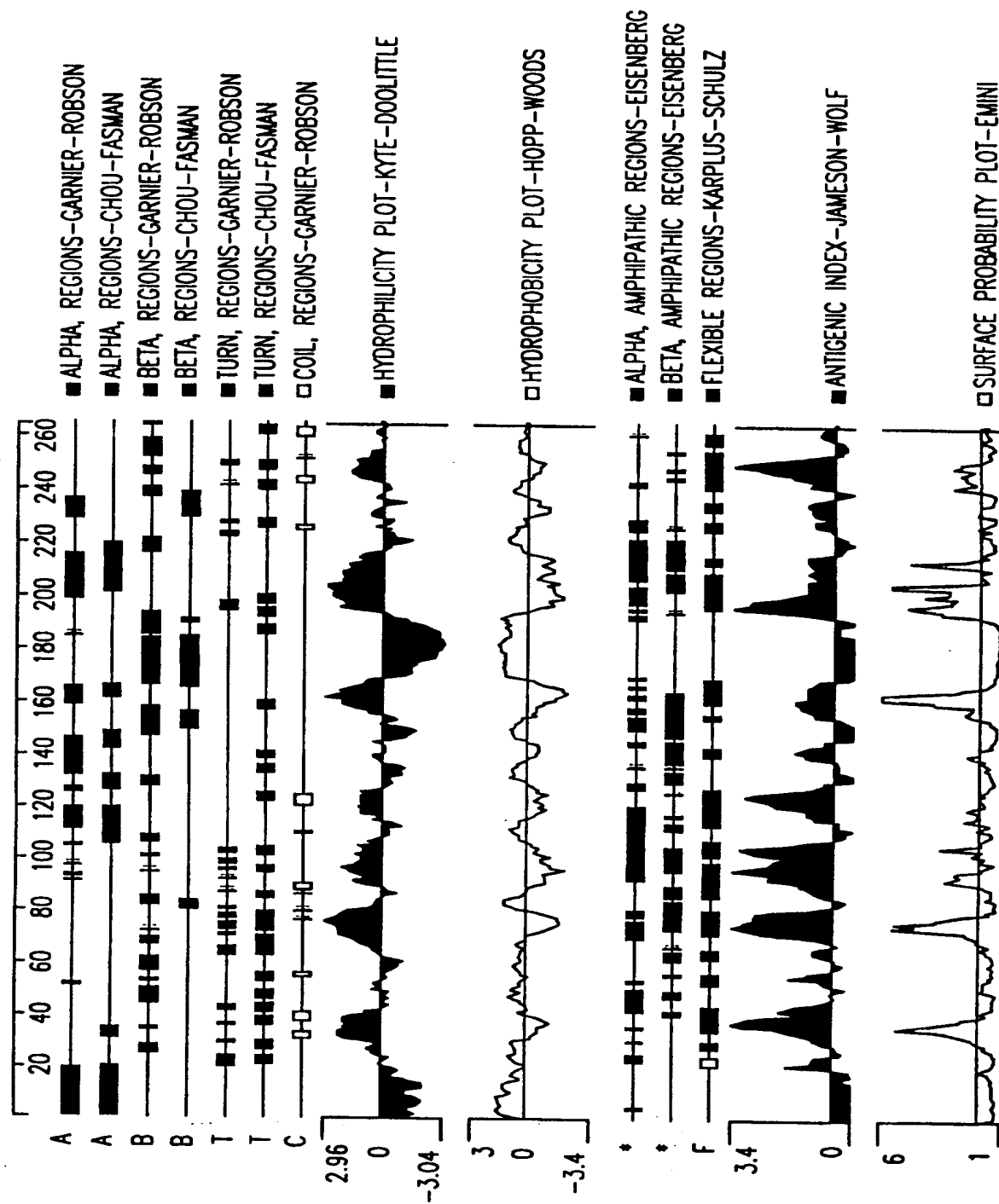


FIG.3

# TUMOR GROWTH OF t-PALP PROTEIN TRANSFECTANTS ON CAM

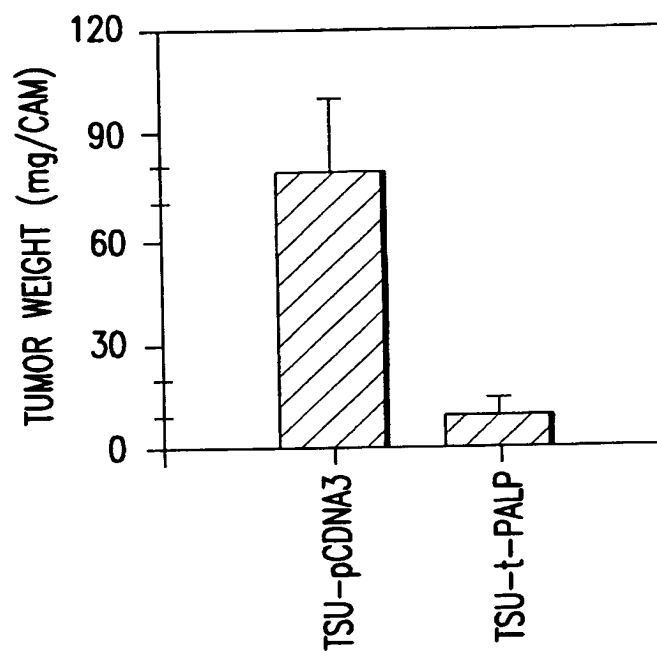


FIG.4

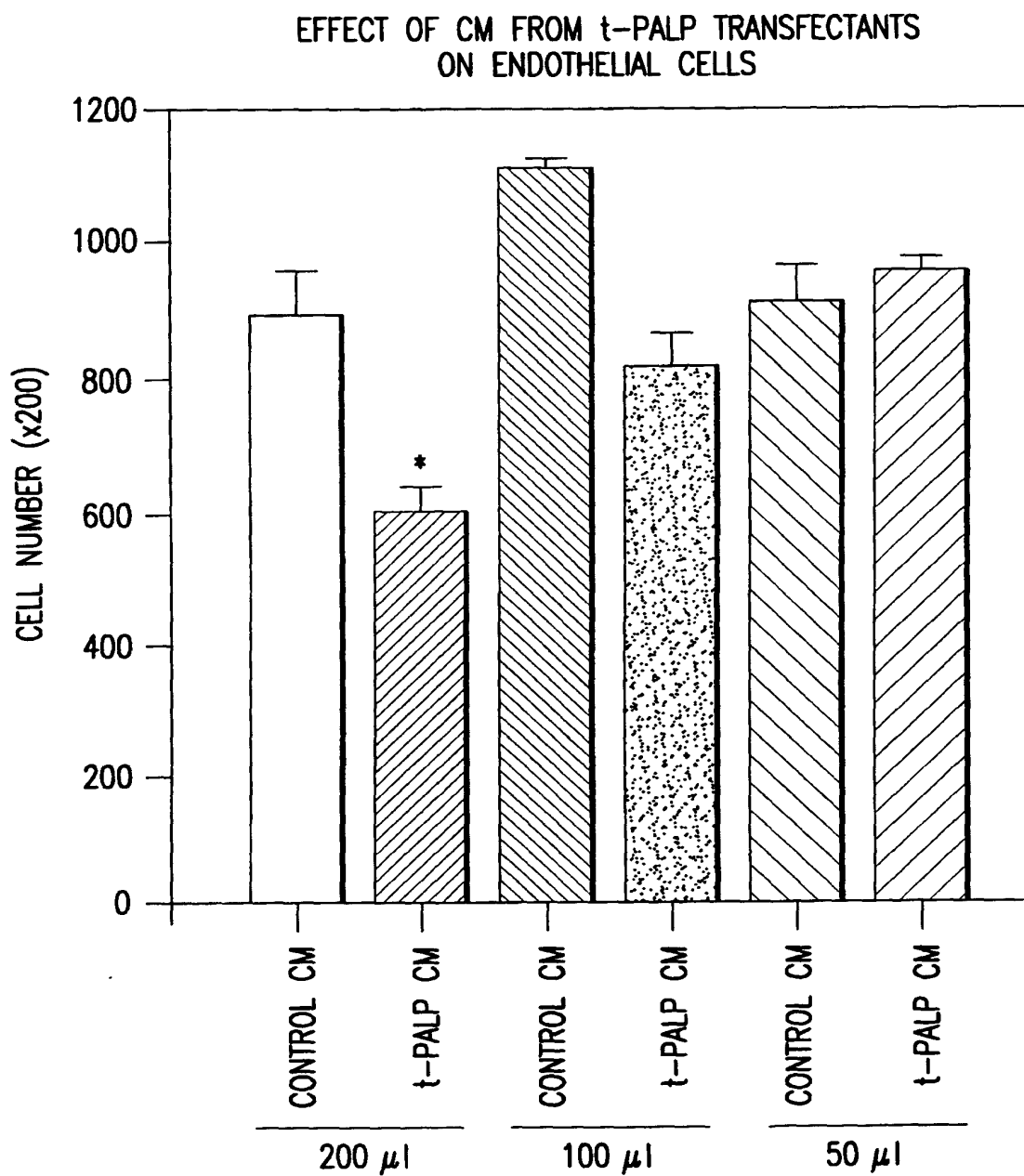


FIG.5

TUMOR GROWTH CURVE OF TSU CELLS TRANSFECTED WITH  
cDNA OF THE t-PALP PROTEIN

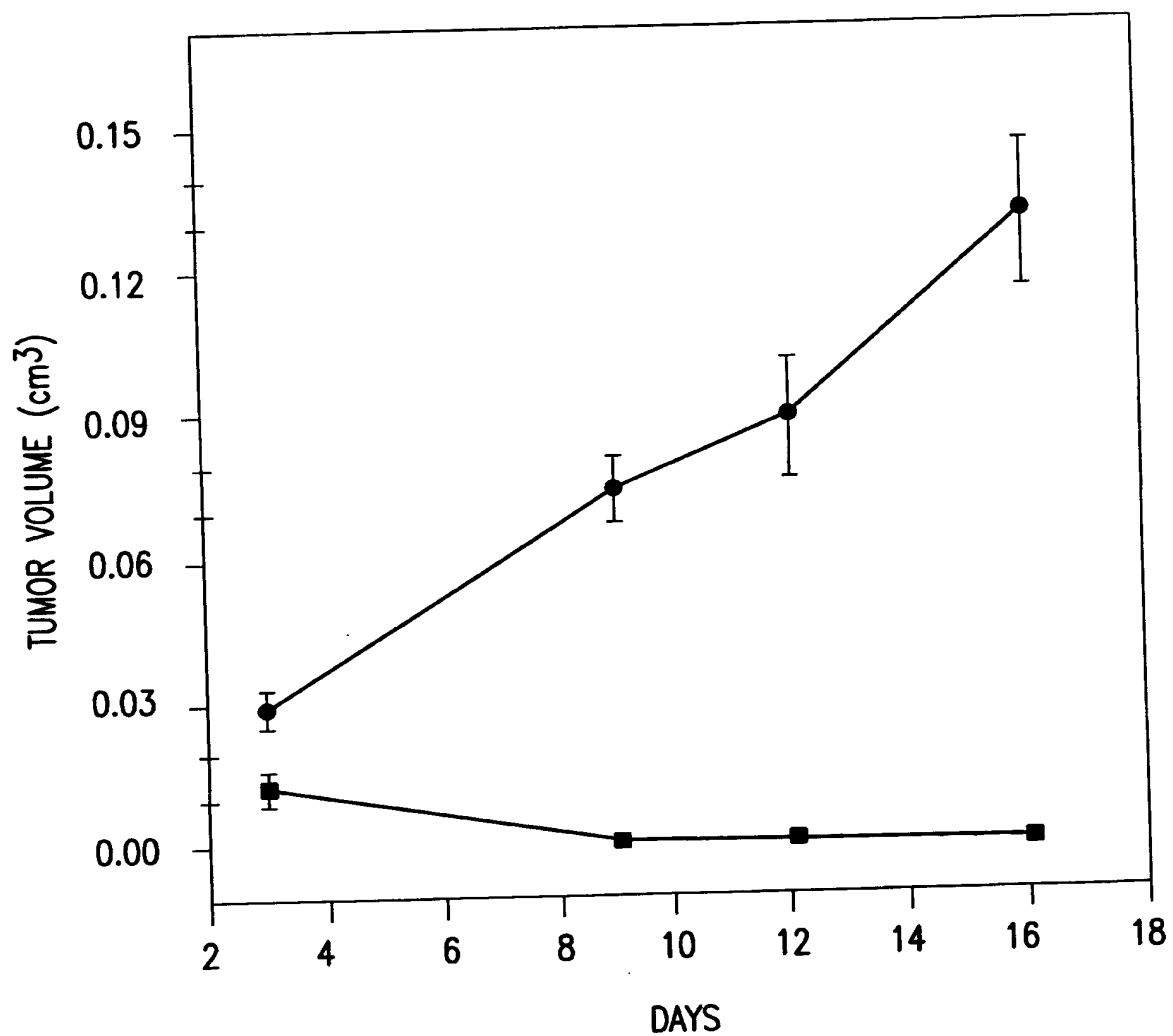


FIG.6